

Figure 1

1 ATGGCTCCCTAGCCGAAGTCGGGGCTTCTGGCGGCCTGGAG
MetAlaProLeuAlaGluValGlyGlyPheLeuGlyGlyLeuGlu
46 GGCTTGGGCCAGCAGGTGGGTTCGCATTCTGTTGCCTCCTGCC
GlyLeuGlyGlnGlnValGlySerHisPheLeuLeuProProAla
91 GGGGAGCGGCCGCGCTGCTGGCGAGCGCAGGAGCGCGGGAG
GlyGluArgProProLeuLeuGlyGluArgArgSerAlaAlaGlu
136 CGGAGCGCGCGCGGGCGGGCTGCGCAGCTGGCGCACCTG
ArgSerAlaArgGlyGlyProGlyAlaAlaGlnLeuAlaHisLeu
181 CACGGCATCCTGCGCCGCGCAGCTCTATTGCCGCACCGGCTTC
HisGlyIleLeuArgArgGlnLeuTyrCysArgThrGlyPhe
226 CACCTGCAGATCCTGCCCGACGGCAGCGTGAGGGCACCCGGCAG
HisLeuGlnIleLeuProAspGlySerValGlnGlyThrArgGln
271 GACCACAGCCTTCGGTATCTTGAATTCACTAGTGTGGCAGTG
AspHisSerLeuPheGlyIleLeuGluPheIleSerValAlaVal
316 GGACTGGTCAGTATTAGAGGTGGACAGTGGTCTCTATCTTGA
GlyLeuValSerIleArgGlyValAspSerGlyLeuTyrLeuGly
361 ATGAATGACAAAGGAGAACTCTATGGATCAGAGAAACTTACTTCC
MetAsnAspLysGlyGluLeuTyrGlySerGluLysLeuThrSer
406 GAATGCATCTTAGGGAGCAGTTGAAGAGAACTGGTATAACACC
GluCysIlePheArgGluGlnPheGluGluAsnTrpTyrAsnThr
451 TATTCATCTAACATATAAACATGGAGACACTGGCCGCAGGTAT
TyrSerSerAsnIleTyrLysHisGlyAspThrGlyArgArgTyr
496 TTTGTGGCACTTAACAAAGACGGAACCTCCAAGAGATGGCGCCAGG
PheValAlaLeuAsnLysAspGlyThrProArgAspGlyAlaArg
541 TCCAAGAGGGCATCAGAAATTACACATTCTTACCTAGACCAGTG
SerLysArgHisGlnLysPheThrHisPheLeuProArgProVal
586 GATCCAGAAAGAGTCCAGAATTGTACAAGGACCTACTGATGTAC
AspProGluArgValProGluLeuTyrLysAspLeuLeuMetTyr
631 ACT
Thr

Figure 2

Query: 170 TGGCGCACCTGCACGGCATCCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACC 229
Sbjct: 2 TGGATCATTAAAGGGATTCTCAGGCAGGACTATACTGCAGGACTGGATTCACT 61

Query: 230 TGCAGATCCTGCCGACGGCAGCGTCAGGGCACCCGGCAGGACACAGCCTTCGGTA 289
Sbjct: 62 TAGAAATCTTCCCAATGGTACTATCCAGGGAACAGGAAAGACCACAGCCGATTGGCA 121

Query: 290 TCTTCCAATTTCAGTGTGCAGTGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTC 349
Sbjct: 122 TTCTGGAATTTCAGTATAGCAGTGGCCTGGTCAGCATTGAGGCGTGGACAGTGGAC 181

Query: 350 TCTATCTTCCAATTGAATGACAAGGAGAACTCTATGGATCAGAGAAACTTACCTCCGAAT 409
Sbjct: 182 TCTACCTCGGGATGAATGAGAAGGGGGAGCTGTATGGATCAGAAAAACTAACCCAAGAGT 241

Query: 410 GCATCTTAGGGAGCAGTTGAAGAGAACTGGTATAACACCTATTCTAACATATATA 469
Sbjct: 242 GTGTATTCAAGAGAACAGTTCGAAGAAAATGGTATAATACGTACTCGTCAAACCTATATA 301

Query: 470 AACATGGAGACACTGGCCGAGGTATTTGTGGCACTTAACAAAGACGGAACCTCAAGAG 529
Sbjct: 302 AGCACGTGGACACTGGAAGGCATACTATGTTGCATTAAATAAGATGGACCCCCGAGAG 361

Query: 530 ATGGCCGCCAGGTCCAAGAGGCATCAGAAATTACACATTCTTACCTAGACCAAGTGGATC 589
Sbjct: 362 AAGGGACTAGGACTAAACGGCACCAGAAATTACACATTACCTAGACCAAGTGGACC 421

Query: 590 CAGA 593
Sbjct: 422 CCGA 425

Figure 3

>gb:GenBank accession number -ID:AB020858|acc:AB020858 Homo sapiens genomic DNA of p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11 - Homo sapiens, 100000 bp.

Minus Strand HSPs:

A.

Score = 1430 (214.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 288/289 (99%), Positives = 288/289 (99%), Strand = Minus / Plus

Query: 289 TACCGAAGAGGCTGTGGTCTGCCGGTGCCCTGCACGCTGCCGTGGCAGGATCTGCA 230
Sbjct: 15927 TACCGAAGAGGCTGTGGTCTGCCGGTGCCCTGCACGCTGCCGTGGCAGGATCTGCA 15986

Query: 229 GGTGGAAGCCGGTGC CGCAATAGAGCTGCCGGCGCAGGATGCCGTGCAGGTGCGCCA 170
Sbjct: 15987 GGTGGAAGCCGGTGC CGCAATAGAGCTGCCGGCG-CGCAGGATGCCGTGCAGGTGCGCCA 16045

Query: 169 GCTGCGCAGCCCCCGGCCGCCGCGCGCTCCGCTCGCCGCCGCTCCGCTCGCCGCCA 110
Sbjct: 16046 GCTGCGCAGCCCCCGGCCGCCGCGCGCTCCGCTCGCCGCCGCTCCGCTCGCCGCCA 16105

Query: 109 GCAGCGGCCGCGCTCCCCGGCAGGAGGAAACAGGAAATGCGAACCCACCTGCTGGCCCA 50
Sbjct: 16106 GCAGCGGCCGCGCTCCCCGGCAGGAGGAAACAGGAAATGCGAACCCACCTGCTGGCCCA 16165

Query: 49 AGCCCTCCAGGCCGCCAGAAAGCCCCGACTTCGGCTAAGGGAGCCAT 1
Sbjct: 16166 AGCCCTCCAGGCCGCCAGAAAGCCCCGACTTCGGCTAAGGGAGCCAT 16214

B.

Score = 1224 (183.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 250/255 (98%), Positives = 250/255 (98%), Strand = Minus / Plus

Query: 633 ATGTACATCAGTAGGTCTTGTACAATTCTGAACTCTTCTGGATCCACTGGCTAGG 574
Sbjct: 7257 ATGTACATCAGTAGGTCTTGTACAATTCTGAACTCTTCTGGATCCACTGGCTAGG 7316

Query: 573 TAAGAAATGTGAAATTCTGATGCCCTTGGACCTGGGCCATCTCTGGAGTTCCGTC 514
Sbjct: 7317 TAAGAAATGTGAAATTCTGATGCCCTTGGACCTGGGCCATCTCTGGAGTTCCGTC 7376

Query: 513 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTATATGTTAGATGA 454
Sbjct: 7377 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTATATGTTAGATGA 7436

Query: 453 ATAGGTGTTATACCAGTTCTCTCAAAC TGCTCCCTAAAGATGCATTGGAAGTAAGTTT 394
Sbjct: 7437 ATAGGTGTTATACCAGTTCTCTCAAAC TGCTCCCTAAAGATGCATTGGAAGTAAGTTT 7496

Query: 393 CTC-TGATCCATAGA 380
Sbjct: 7497 CTCCTGAAAGAGAGA 7511

Figure 3 (cont.)

C.

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Score = 530 (79.5 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
  Identities = 106/106 (100%), Positives = 106/106 (100%), Strand = Minus / Plus

Query:   391 CTGATCCATAGAGTTCTCCTTGTCAATTCAAGATAGAGACCACTGTCCACACCTC 332
          ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:  9837 CTGATCCATAGAGTTCTCCTTGTCAATTCAAGATAGAGACCACTGTCCACACCTC 9896

Query:   331 TAATACTGACCAGTCCCCTGCCACACTGATGAATTCCAAGATACC 286
          ||||||| | | | | | | | | | | | | | | | | | | | | |
Sbjct:  9897 TAATACTGACCAGTCCCCTGCCACACTGATGAATTCCAAGATACC 9942

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Figure 4

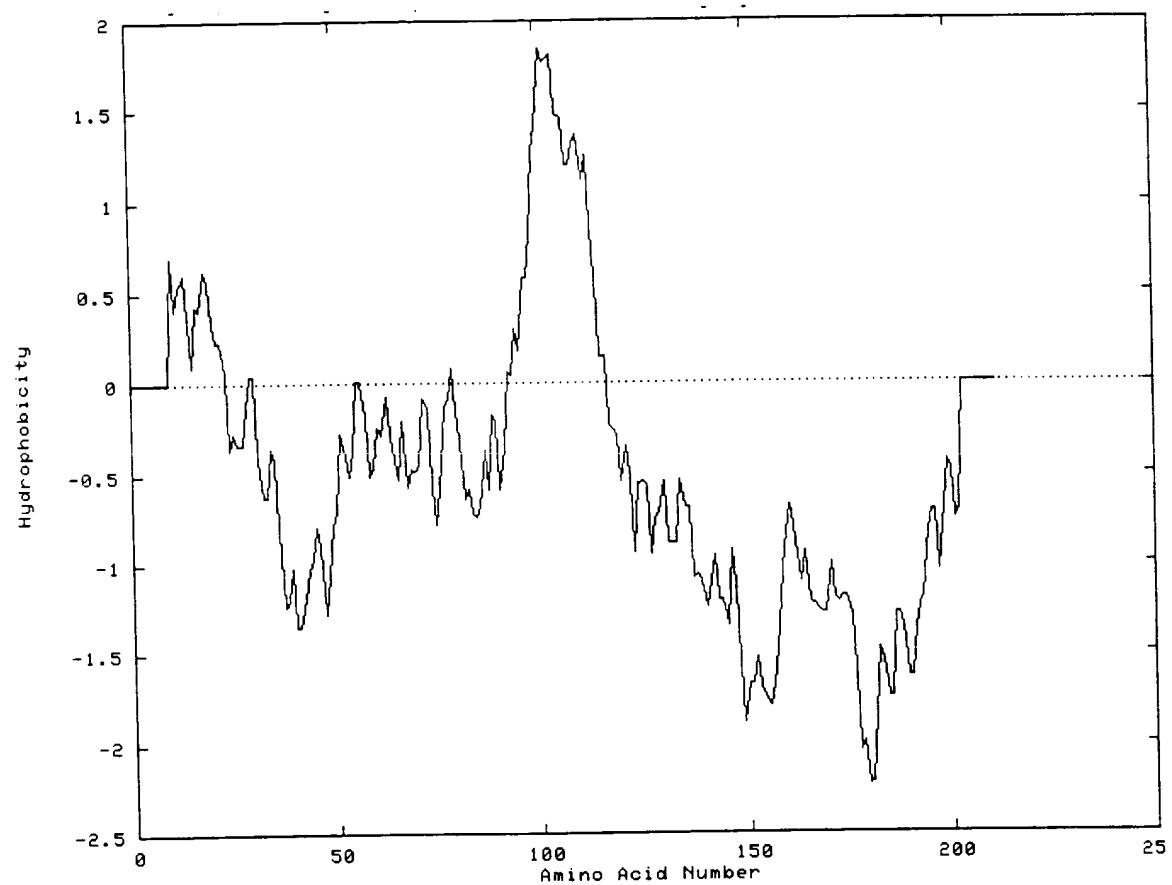


Figure 5

ptnr:SWISSPROT-ACC:P31371 GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9) (FGF-9) (HBGF-9) - HOMO SAPIENS (HUMAN), 208 aa. Identities = 147/208 (70%), Positives = 170/208 (81%)

Query: 1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPAGERPPLLGERRSAERSARG-GPGAAQLAH 59
||||| |||| + | + + | + +||| + | || + +| || | | | |
Sbjct: 1 MAPLGEVGNYFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH 56

Query: 60 LHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILEFISAVGLVSIRGVDSGLYL 119
| |||||||||||||||+| |+|++||||+|||| ||||||||+|||||||||||||
Sbjct: 57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRGILEFISIAVGLVSIRGVDSGLYL 116

Query: 120 GMNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
||||+||||||||| | |+||||||||| |+|||| | | | |+| | | | | |+|
Sbjct: 117 GMNEKGELYGSEKLTQECSVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTPREGT 176

Query: 180 RSKRHQKFTHFLPRPVDPERVPELYKDLL 208
|+||||||||| | | | |+| | | | |+|
Sbjct: 177 RTKRHQKFTHFLPRPVDPDKVPELYKDIL 205

Figure 6

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

Query:	1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERRSAERSARG-GPGAAQLAH 59
	+ + + + + + + +
Sbjct:	1 MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLNDHLGQSEAGGLPRGPAVTLDH 56
Query:	60 LHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILEFISAVGLVSIRGVDSGLYL 119
	+ + ++ + + +
Sbjct:	57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRGILEFISIAVGLVSIRGVDSGLYL 116
Query:	120 GMNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
	+ + + + + +
Sbjct:	117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTPREGT 176
Query:	180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
	+ + + +
Sbjct:	177 RTKRHQKFTHFLPRPVDPDKVPELYKDIL 205

Figure 7

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

Query:	1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
	+ + + + + + +
Sbjct:	1 MAPLGEVGSYFGVQDAV--PFGNVPVLV--DSPVLLSDHLGQSEAGGLPRGPAVTLDH 56
Query:	60 LHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILEFISAVGLVSIRGVDSGLYL 119
	+ + + +
Sbjct:	57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRGILEFISIAVGLVSIRGVDSGLYL 116
Query:	120 GMNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
	+ + + +
Sbjct:	117 GMNEKGELYGSEKLTQECSVFREQFEENWYSSNLYKHVDTGRRYYVALNKDGTPREGT 176
Query:	180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
	+ + +
Sbjct:	177 RTKRHQKFTHFLPRPVDPDKVPELYKDIL 205

Figure 8

FGF-CX Query Length = 211
XFGF-20 Sbjct Length = 208

Plus Strand HSPs:

Score = 906 (318.9 bits), Expect = 4.4e-90, P = 4.4e-90
Identities = 170/211 (80%), Positives = 189/211 (89%), Frame = +1

Query: 1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPAGERPPLLGERRSAAERSARGGPGAAQLAHL 60
Sbjct: 1 MAPLADVGTFLGGYDALGQ-VGSHFLLPPAKDSPLLFDPLAQSERLSRSAP--SDLSHL 57

Query: 61 HGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILEFISVAVGLVSIRGVDSGLYLG 120
Sbjct: 58 QGILRRRQLYCRTGFHLQILPDGNVQGTRQDHSRFGILEFISVAIGLVSIRGVDTGLYLG 117

Query: 121 MNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGAR 180
Sbjct: 118 MNDKGELFGSEKLTSECIFREQFEENWYNTYSSNLYKHGDSGRYYFVALNKDGTPRDGTR 177

Query: 181 SKRHQKFTHFLPRPVDPERVPVELYKDLMYT 211
Sbjct: 178 AKRHQKFTHFLPRPVDPPEKVPVELYKDLMGYS 208

FIGURE 9

Sequences analyzed:

1. HUMAN FGF-9 (P31371_HUMAN FGF-9) [SEQ ID NO:9]
2. MOUSE FGF-9 (P54130_MOUSE FGF-9) [SEQ ID NO:10]
3. RAT FGF-9 (P36364_FGF9_RAT FGF-9) [SEQ ID NO:11]
4. XENOPUS XFGF-20 (BAA83474Xen; Xenopus laevis XFGF-20) [SEQ ID NO:12]
5. FGF-CX (cgAB020858) [SEQ ID NO:2]

Multiple Alignment:

HUMAN FGF-9	M A P L G E V G N Y F G V Q D A V P -	- F G N V P V L P -	- V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
RAT FGF-9	M A P L G E V G S Y F G V Q D A V P -	- F G N V P V L P -	- V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
MOUSE FGF-9	M A P L G E V G S Y F G V Q D A V P -	- F G N V P V L P -	- V D S P V L L N D H L G Q S E A G G L P R G P A V T D L D H
XENOPUS XFGF-20	M A P L A D V G T F L G G Y D A I L G - Q V G G S H F L L P P A K D S P H I E N D P L A Q S E R L S R - S E P -	- S D L S H	
FGF-CX	M A P L A E V G G F F L G G L E G G L G Q Q V G S H F L L P P A G E R P P L L G E R R S A E R S A R - G C P G A A Q L A H		
HUMAN FGF-9	L K G I L R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L		
RAT FGF-9	L K G I L R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L		
MOUSE FGF-9	L K G I L R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L		
XENOPUS XFGF-20	L Q G I L R R Q L Y C R T G F H L Q I L P D G N V Q G G T R Q D H S R F G I L E F I S I V A T I G L V S I R G V D S G L Y L		
FGF-CX	L H G I L R R Q L Y C R T G F H L Q I L P D G S V Q G G T R Q D H S L F G I L E F I S I V A V G L V S I R G V D S G L Y L		
HUMAN FGF-9	G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T		
RAT FGF-9	G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T		
MOUSE FGF-9	G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R D G T		
XENOPUS XFGF-20	G M N D K G E L F G S E K L T S E C T I F R E Q F E E N W Y N T Y S S N T Y K H G D T G R R Y F V A L N K D G T P R D G A		
FGF-CX	G M N D K G E L Y G S E K L T S E C T I F R E Q F E E N W Y N T Y S S N T Y K H G D T G R R Y F V A L N K D G T P R D G A		
HUMAN FGF-9	R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S		
RAT FGF-9	R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S		
MOUSE FGF-9	R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S		
XENOPUS XFGF-20	R A K R H Q K F T H F L P R P V D P E K V P E L Y K D I L M G Y S		
FGF-CX	R S K R H Q K F T H F L P R P V D P E R V P E L Y K D I L M Y T		